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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/866,987

DATE: 10/29/2001

TIME: 15:28:17

Input Set : A:\38621180.app

Output Set: N:\CRF3\10292001\I866987.raw

3 <110> APPLICANT: PLOWMAN, GREGORY D.

4 MARTINEZ, RICARDO

5 WHYTE, DAVID

6 MANNING, GERARD

7 SUDARSANAM, SUCHA

8 CAENEPEEL, SEAN

9 HILL, RON

10 FLANAGAN, PETER

12 <120> TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES

14 <130> FILE REFERENCE: 038602/1180

16 <140> CURRENT APPLICATION NUMBER: 09/866,987

17 <141> CURRENT FILING DATE: 2001-05-30

19 <150> PRIOR APPLICATION NUMBER: 60/208,291

20 <151> PRIOR FILING DATE: 2000-05-30

22 <160> NUMBER OF SEQ ID NOS: 17

24 <170> SOFTWARE: PatentIn Ver. 2.1

26 <210> SEQ ID NO: 1

27 <211> LENGTH: 1026

28 <212> TYPE: DNA

29 <213> ORGANISM: Artificial Sequence ✓

31 <220> FEATURE:

32 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic ✓

33 phosphatase nucleotide

35 <400> SEQUENCE: 1

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36 agtggtttc accccaacat cagcagggtg gaggcggaga agctgttctt atccagaggt 60
37 cagcgtgggg acttccttgc caggcccagt gagagcagcc cggggggctt cacgctgtcc 120
38 gtcagagagg cccttgggga gggtcattg agtcaggggc tcagcaggac ctttctctcc 180
39 cctgtgaggg ccctggggac aggcagggcc tccgtggctg cgaccgtgtt gccagagcct 240
40 gggggtgcag ctggggagtg cagcgggggtt cccattgagc tctggtacct gctgggctgc 300
41 caggaccccc cgttggagtg gtggtaccac gggcgccctgt ctggcaagga ggctgagaag 360
42 ctgctgctgc agaaggggca tccgggcagc ttcctgggtg acatgagtca gagcgatcct 420
43 gggggcttcc cgctgtcagc gctgacgcaa ggggtgggacg aggcgcaggg ctcaggccgc 480
44 cagccacagg tcacgcacat catgactcac tcccagggtg gagggggcgg cgagctgggg 540
45 cggcctctgg gaagggcggg cggccttggc caggcccttc accgccacc ccacggccgg 600
46 atgagaagtc tctccctgca gccctcaag gccacagga tcagtgtctg gagcctggag 660
47 ggctgtgtgc aggagagcag ggccactgat gccagcggga aggccaggca gggcttcttg 720
48 gtggagttca agatgtctga gcagcaggaa tgccgggttc tgtaccctcg gaaggagggg 780
49 cagagtgtgg agaacaagcc caagaatcac tacaagaaca tccttccctg tgagggcgga 840
50 ggccaggcgg tcacccgtcg ggcctggggg agggcctcgc gggcgaggg tgtacatcgc 900
51 ctgcagggct gtctgcaggc ctgtctgcag gccacgggtg ctgcttctg ggcacgggtg 960
52 caccaggaga acacgcgtgt catcgtcatg accaccagg agatggagcg gggccgggta 1020
53 ggggtg                                     1026

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56 <210> SEQ ID NO: 2

57 <211> LENGTH: 800

58 <212> TYPE: DNA

59 <213> ORGANISM: Artificial Sequence ✓

61 <220> FEATURE:

ENTERED

ENTERED

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62 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

63 phosphatase nucleotide

65 <400> SEQUENCE: 2

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66 gctccgaggc cgccgggccc tctccagag tcccgccagt ccccagagt ccaggccagt 60
67 ccccgccgtc acccggtgcg aaccgcgcag aggcctagtg cagctggcag ccccgccccg 120
68 gcaccgcct gctcttctcg cgggtccgga ccgcgagcgc gggggccgac gggtcgcgc 180
69 tgcgcgggc cgggatggcg gccaccgcgc tgcctggaggc cggcctggcg cgggtgctct 240
70 tctaccgcac gctgctctac accctgttcc gcgggaaggt gccgggtcgg gcgcaccggg 300
71 actggtacca ccgcacgcac cccaccgtgc tgcctgggcgc gctgccgttg cggagcttga 360
72 cgcgcagct ggtacaggac gagaacgtgc gcggggtgat caccatgaac gaggagtacg 420
73 agacgaggtt cctgtgcaac tcttcacagg agtggaagag actaggagtc gagcagctgc 480
74 ggtcagcac agtagacatg actgggatcc ccaccttga caacctccag aaggagatcc 540
75 aatttgcct caagtaccag tcgctgggccc agtgtgttta cgtgcattgt aaggctgggc 600
76 gctccaggag tgccactatg gtggcagcat acctgattca ggtgcacaaa tggagtccag 660
77 aggaggctgt aagagccatc gccaaagatcc ggtcatacat ccacatcagg cctggccagc 720
78 tggatgttct taaagagttc cacaagcaga ttactgcacg ggcaacaaag gatgggactt 780
79 ttgtcatttc aaagacatga
800

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82 <210> SEQ ID NO: 3

83 <211> LENGTH: 1380

84 <212> TYPE: DNA

85 <213> ORGANISM: Artificial Sequence

87 <220> FEATURE:

88 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

89 phosphatase nucleotide

91 <400> SEQUENCE: 3

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92 atgtccgccc gctgggttccg gcgcgcgttc ctgcctgggg agccgtctcc cgcgcgcgcg 60
93 ccgcctgggc cgcgtgccag ccccggtgcc taccgacggc cccgcttcc tgcgggtccc 120
94 agctccagcc ccggggcggc cgacgcctcg cgcgcgccag actcccgccc cgtgcgcagc 180
95 ccgcacagag gacgcacgct accctggaat gcaggctacg ccgagattat caatgcagag 240
96 aaatctgaat tcaatgagga tcaagccgcc tgtgggaagc tgtgcatccg gagatgtgag 300
97 tttggggctg aagaagagtg gctgaccctg tgcccagagg agttcctgac aggccattac 360
98 tgggcaactg tcgatgggca cggcgggtcc gcagcagcca tcttggctgc caacacctg 420
99 cactcctgct tgcgccggca gctggaggcc gtggtggaag gcttgggtgg cactcagccc 480
100 cccatgcacc tcaatggccc ctgcatctgc cccagtgacc ctgagtttgt ggaggaaaag 540
101 ggcacaggg cagaagactt ggtgatcggg gcattggaga gtgcctttca ggaatgtgat 600
102 gaggtgatcg ggcgggagct ggaggcctca ggccagatgg gcggctgcac agccctgggt 660
103 gctgtgtccc tgcagggaaa gctgtacatg gccaatgctg gggatagcag ggccatcttg 720
104 gtgcggagag atgagatacg gccactgagc ttcgagttca cccagagac tgagcggcag 780
105 cggatccagc agctggcctt tgtctatcct gagcttctgg ctggtgagtt caccgcactg 840
106 gagttccctc gcgggctgaa gggggatgac ttgggacaga aggttttgtt cagggatcac 900
107 cacatgagtg gctggagcta caaacgtgtg gagaaatcgg atctcaagta cccactgac 960
108 catggacagg gtaggcaggc tcggttacta ggaacactgg ctgtctcccg gggcctggga 1020
109 gaccatcagc tcagagtcct ggacacaaac atccagctca agcccttctt gctctctgtg 1080
110 ccacaggtga ctgtgctgga tgtggaccag ctggagctac aggaggatga tgtggttgtc 1140
111 atggcaactg atggactctg ggatgtactg tccaacgagc aggtggcatg gctggtgcgg 1200
112 agcttctctc ctgggaacca agaggaccca cacaggttct caaagctggc ccagatgctg 1260
113 atacacagca cacagggaag ggaagacagt ctacacagag aagggcaggt gtccatcgat 1320
114 gacgtctctg tgttcgtgat tcccttgca agtcaggggc aagagagcag tgaccaactga 1380
117 <210> SEQ ID NO: 4

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118 <211> LENGTH: 1164
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
124     phosphatase nucleotide
126 <400> SEQUENCE: 4
127 atgagagcgt ggatccctgg gtgggttggg cggccgcacg ggggtgccga ggcgtctggg 60
128 ggctgcgct tcggggcgag cgcagcgcaa ggctggcgcg cgcgcatgga ggatgctcac 120
129 tgcacttggc ttctgttacc tggcttgccc cgggctggg ccttgtttgc cgtcctcgac 180
130 ggcacgggtg gggctcgagc tgcccgttcc ggtgcacgcc atttgccagg ccatgtgctc 240
131 caggagctgg gcccgagacc tagcgagccc gagggcgtgc gcgaggcgt gcgccgagcc 300
132 ttcttgagcg ccgacgagcg ccttcgctcc ctctggcccc gcgtggaaac gggcggcttc 360
133 acggccgtag tgttgctggg cccccgcgg tttctgtacc tggcgactg cggtgactcc 420
134 cgcgcggtgc tgagccgcgc tggcgccgtg gccttcagca cagaggacca ccggccccctt 480
135 cgaccccggg aacgcgagcg catccacgcc gctggcggca ccacccgcg ccgcgcgctc 540
136 gagggctctc tggccgtgtc gcgagcgttg ggcgacttta cctacaagga ggctccgggg 600
137 agggcccccg agctacagct cgtttctgcg gagccagagg tggccgcact ggcacgccag 660
138 gctgaggacg agttcatgct cctggcctct gatggcgtct gggacactgt gtctggtgct 720
139 gccctggcgg gactggtggc ttacgcctc cgcttgggcc tggccccaga gttctctgc 780
140 gcgcagctgt tggacacgtg tctgtgcaag ggcagcctgg acaacatgac ctgcactctg 840
141 gtctgcttcc ctggggcccc taggccttct gaggaggcga tcaggaggga gctagcactg 900
142 gacgcagccc tgggctgcag aatcgctgaa ctgtgtgct ctgctcagaa gccccccagc 960
143 ctgaacacag ttttcaggac tctggcctca gaggacatcc cagatttacc tcctggggga 1020
144 gggctggact gcaaggccac tgtcattgct gaagtttatt ctcatctg ccaggtctca 1080
145 gaagagtgcg gagagaaggg gcaggatggg gctgggaagt ccaacccac gcatttgggc 1140
146 tcagccttgg acatggaggc ctga                                     1164
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150 <211> LENGTH: 429
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
156     phosphatase nucleotide
158 <400> SEQUENCE: 5
159 ttaggtaatg tgcaagcagt cttatgcaga aatgggaaag gtttttgctt aaccaaagaa 60
160 cactactacac gaaacacaaa tgaaagaaga agaatacttc agaatggagc agtcattagt 120
161 tcaaatgaac catacgggct tgtagagggg caagtaaaaa ctacacgagg acttgatttt 180
162 catggaaaac tcaagctgaa aaaatccatt atcccagcac ctcaaactat ttctgtccct 240
163 atagatgacc tatgtcaatt cttattgta gctactaatg gactttggga agttttggat 300
164 aaagagggaag ttgatgtggc aacaaatgaa aaagaatcag acactaagag tttctatgaa 360
165 ggcgcagctg agtatgttag ccatgaactt gtaaatgctg ctttactggc tggctccaga 420
166 gacaacatt                                     429
169 <210> SEQ ID NO: 6
170 <211> LENGTH: 342
171 <212> TYPE: PRT
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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176      phosphatase polypeptide
178 <400> SEQUENCE: 6
179 Arg Trp Phe His Pro Asn Ile Ser Arg Val Glu Ala Glu Lys Leu Phe
180   1          5          10          15
182 Leu Ser Arg Gly Gln Arg Gly Asp Phe Leu Ala Arg Pro Ser Glu Ser
183          20          25          30
185 Ser Pro Gly Gly Phe Thr Leu Ser Val Arg Glu Ala Leu Gly Glu Gly
186          35          40          45
188 Ser Leu Ser Gln Gly Leu Ser Arg Thr Leu Ser Ser Pro Val Arg Ala
189          50          55          60
191 Leu Gly Thr Gly Arg Ala Ser Val Ala Ala Thr Val Leu Pro Glu Pro
192  65          70          75          80
194 Gly Gly Ala Ala Gly Glu Cys Ser Gly Val Pro Ile Glu Leu Trp Tyr
195          85          90          95
197 Pro Leu Gly Cys Gln Asp Pro Ala Leu Glu Trp Trp Tyr His Gly Arg
198          100         105         110
200 Leu Ser Gly Lys Glu Ala Glu Lys Leu Leu Leu Gln Lys Gly His Pro
201          115         120         125
203 Gly Ser Phe Leu Val His Met Ser Gln Ser Asp Pro Gly Gly Phe Pro
204          130         135         140
206 Leu Ser Ala Leu Thr Gln Gly Trp Asp Glu Ala Gln Gly Ser Gly Arg
207 145         150         155         160
209 Gln Pro Gln Val Thr His Ile Met Thr His Ser Gln Val Gly Gly Gly
210          165         170         175
212 Gly Glu Leu Gly Arg Pro Leu Gly Arg Ala Gly Gly Leu Gly Gln Ala
213          180         185         190
215 Pro His Arg His Pro His Gly Arg Met Arg Ser Leu Ser Leu Gln Pro
216          195         200         205
218 Leu Lys Ala Thr Arg Ile Ser Ala Arg Ser Leu Glu Gly Cys Val Gln
219          210         215         220
221 Glu Ser Arg Ala Thr Asp Ala Ser Gly Lys Ala Arg Gln Gly Phe Trp
222 225         230         235         240
224 Val Glu Phe Lys Met Leu Gln Gln Gln Glu Cys Arg Phe Leu Tyr Pro
225          245         250         255
227 Arg Lys Glu Gly Gln Ser Val Glu Asn Lys Pro Lys Asn His Tyr Lys
228          260         265         270
230 Asn Ile Leu Pro Cys Glu Gly Gly Gln Gly Val Thr Arg Arg Ala
231          275         280         285
233 Trp Gly Arg Ala Ser Arg Ala Gln Gly Val His Arg Leu Gln Gly Cys
234          290         295         300
236 Leu Gln Ala Cys Leu Gln Ala Thr Val Ala Ala Phe Trp Ala Thr Val
237 305         310         315         320
239 His Gln Glu Asn Thr Arg Val Ile Val Met Thr Thr Arg Glu Met Glu
240          325         330         335
242 Arg Gly Arg Val Gly Val
243          340
246 <210> SEQ ID NO: 7
247 <211> LENGTH: 201
248 <212> TYPE: PRT

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249 <213> ORGANISM: Artificial Sequence

251 <220> FEATURE:

252 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic ✓

253 phosphatase polypeptide

255 <400> SEQUENCE: 7

256 Met Ala Ala Thr Ala Leu Leu Glu Ala Gly Leu Ala Arg Val Leu Phe

257 1 5 10 15

259 Tyr Pro Thr Leu Tyr Thr Leu Phe Arg Gly Lys Val Pro Gly Arg

260 20 25 30

262 Ala His Arg Asp Trp Tyr His Arg Ile Asp Pro Thr Val Leu Leu Gly

263 35 40 45

265 Ala Leu Pro Leu Arg Ser Leu Thr Arg Gln Leu Val Gln Asp Glu Asn

266 50 55 60

268 Val Arg Gly Val Ile Thr Met Asn Glu Glu Tyr Glu Thr Arg Phe Leu

269 65 70 75 80

271 Cys Asn Ser Ser Gln Glu Trp Lys Arg Leu Gly Val Glu Gln Leu Arg

272 85 90 95

274 Leu Ser Thr Val Asp Met Thr Gly Ile Pro Thr Leu Asp Asn Leu Gln

275 100 105 110

277 Lys Gly Val Gln Phe Ala Leu Lys Tyr Gln Ser Leu Gly Gln Cys Val

278 115 120 125

280 Tyr Val His Cys Lys Ala Gly Arg Ser Arg Ser Ala Thr Met Val Ala

281 130 135 140

283 Ala Tyr Leu Ile Gln Val His Lys Trp Ser Pro Glu Glu Ala Val Arg

284 145 150 155 160

286 Ala Ile Ala Lys Ile Arg Ser Tyr Ile His Ile Arg Pro Gly Gln Leu

287 165 170 175

289 Asp Val Leu Lys Glu Phe His Lys Gln Ile Thr Ala Arg Ala Thr Lys

290 180 185 190

292 Asp Gly Thr Phe Val Ile Ser Lys Thr

293 195 200

296 <210> SEQ ID NO: 8

297 <211> LENGTH: 459

298 <212> TYPE: PRT

299 <213> ORGANISM: Artificial Sequence

301 <220> FEATURE:

302 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic ✓

303 phosphatase polypeptide

305 <400> SEQUENCE: 8

306 Met Ser Ala Gly Trp Phe Arg Arg Arg Phe Leu Pro Gly Glu Pro Leu

307 1 5 10 15

309 Pro Ala Pro Arg Pro Pro Gly Pro His Ala Ser Pro Val Pro Tyr Arg

310 20 25 30

312 Arg Pro Arg Phe Leu Arg Gly Ser Ser Ser Ser Pro Gly Ala Ala Asp

313 35 40 45

315 Ala Ser Arg Arg Pro Asp Ser Arg Pro Val Arg Ser Pro Ala Arg Gly

316 50 55 60

318 Arg Thr Leu Pro Trp Asn Ala Gly Tyr Ala Glu Ile Ile Asn Ala Glu

319 65 70 75 80

Use of n and/or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa

VERIFICATION SUMMARY

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L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11